





```

Query Match          25.9%; Score 92; DB 2; Length 810;
Best Local Similarity 36.4%; Pred. No. 0.031;
Matches 24; Conservative 11; Mismatches 23; Indels 8; Gaps 3;

OY      1 KRDPQREYEDCDRRRCEDQEE--PQQHOCQLCRFE--QQRHGRGSDMMNPFQGGSGRYE 56
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      70 QNGSPRAYEYVCRLRQGYAERKVEQQRKCEQYCEERLREREGQKEDYDEVER-----RDP 125
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      57 EGGEEO 62
      | | | | |
Db      126 EWEREE 131

RESULT      7
T13998
gene mastermind protein - fruit fly (Drosophila virilis)
C:Species: Drosophila virilis
C:Date: 20-Sep-1999 #sequence-revision 20-Sep-1999 #text-change 20-Sep-1999
C:Accession: T13998
R:Newfeld, S.J.; Tachida, H.; Yedvobnick, B.
J. Mol. Evol. 38, 637-641, 1994
A:Title: Drive-selection equilibrium: homopolymer evolution in the Drosophila gene mastermind
A:Reference number: Z17850; MUID:943365848
A:Accession: T13998
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1655 <NEM>
A:Cross-references: EMBL:M92914; NID:g157833; PID:g157834; PIDN:AAC37201.1

```

Query Match 24.2% Score 86; DB 2; Length 1655;  
 Best Local Similarity 32.8% Pred. No. 0.25;  
 Matches 19; Conservative 16; Mismatches 17; Indels 6; Gaps 2;

RESULT 8  
 S25365  
 CYC8 protein - yeast (*Saccharomyces cerevisiae*)  
 N:Alternate names: glucose repression mediator; protein YBR0908; protein YBR112c; SSN6  
 C:Species: *Saccharomyces cerevisiae*  
 C:Date: 17-Apr-1993 #sequence, revision 17-Apr-1993 #text\_change 11-Jan-2000  
 C:Accession: S25365; S48277; S45980; S25404; S25405; A30906; S44692  
 R:Mannhaupt, G.; Stucka, R.; Ehmlé, S.; Vetter, I.; Feldmann, H.  
 Yeast 8, 397-408, 1992  
 A>Title: Molecular analysis of yeast chromosome II between CMD1 and LYS2: the excision  
 A:Reference number: S25364; MUID:92327848  
 A:Molecule type: DNA  
 A:Residues: 1-966 <MAN>  
 A:Cross-references: EMBL:X66247; NID:93548; PIDN:CAA46973.1; PID:93550  
 R:Mannhaupt, G.; Stucka, R.; Ehmlé, S.; Vetter, I.; Feldmann, H.  
 Yeast 10, 1363-1381, 1994  
 A>Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.  
 A:Reference number: S48255; MUID:95208357  
 A:Accession: S48277  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-966 <MAN>  
 A:Cross-references: EMBL:X78993; NID:9476045; PIDN:CAA55615.1; PID:9476068  
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994  
 R:Feldmann, H.; Mannhaupt, G.; Schwarlose, C.; Vetter, I.  
 submitted to the Protein Sequence Database, August 1994  
 A:Reference number: S45927  
 A:Accession: S45980  
 A:Molecule type: DNA  
 A:Residues: 1-966 <FE2>  
 A:Cross-references: EMBL:Z35981; NID:9536449; PIDN:CAA85069.1; PID:9536450; MIPS:YBR112D

R:Schultz, J., Carlson, M.  
Mol. Cell. Biol. 7, 3637-3645, 1987

A:Title: Molecular analysis of SSN6, a gene functionally related to the SMF1 protein  
A:Reference number: S25404; MUID:88065502

A:Accession: S25404

A:Molecule type: DNA

A:Residues: 1-546; 'K', 548-966 <SCH>

A:Cross-references: EMBL:M17826; NID:g172725; PIDN:AAA35103.1; PID:g172726

R:Trumbly, R.J.  
Gene 73, 97-111, 1988

A:Title: Cloning and characterization of the CYC8 gene mediating glucose repression i  
A:Reference number: S25405; MUID:89211964

A:Accession: S25405

A:Molecule type: DNA

A:Residues: 1-546; 'K', 548-966 <TRU>

A:Cross-references: EMBL:M2440; NID:g171349; PIDN:AAA34545.1; PID:g171350

C:Genetics:

A:Gene: SGD:CYC8; SSN6; CRT8

A:Cross-references: SGD:S0000316; MIPS:YBR112C

A:Map position: 2R

C:Function:

C:Description: required for complete derepression of ICL1; required for repression of  
C:Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat  
C:Keywords: nucleus; transcription regulation

F:224-257/Domain: tetratricopeptide repeat homology <TT1>  
F:262-295/Domain: tetratricopeptide repeat homology <TT2>  
F:266-329/Domain: tetratricopeptide repeat homology <TT3>  
F:330-363/Domain: tetratricopeptide repeat homology <TT4>  
F:365-398/Domain: tetratricopeptide repeat homology <TT5>

Query Match 23.7%; Score 84; DB 2; Length 966;  
Best Local Similarity 34.0%; Pred. No. 0.25;  
Matches 17; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

```
QY      1 KRDPQREYEDRCRCEDEQEPRHQHCQLRCHEGRGROHGRGDMMNPPRG 50  
Db     :|||||:||||:||||:||||:||||:||||:||||:||||:||||: 11111:  
562 0000000000000000000000000000000000LPLPRPQQLDQKGVSYQMNPQG 611
```

RESULT 9  
T01662  
gloabulin-1 - maize (fragment)  
C:Species: Zea mays (maize)  
C:Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 11-Jan-2000  
C:Accession: T01662  
R:Hilton, H.; Gaut, B.S.  
Genetics 150, 863-872, 1998  
A:Title: Speciation and domestication in maize and its wild relatives: evidence from  
A:Reference number: Z14386; MUII:98429537  
A:Accession: T01662  
A:Status: preliminary; translated from GR/EMBL/DBJ  
A:Molecule type: DNA  
A:Residue: 1-236 (#HL>  
A:Cross-references: EMBL:AF064222; NID:g3414836; PIDN:AAC31465.1; PID:g3414837  
A:Experimental source: subspecies parviglumis  
C:Genetics:  
A:Introns: 166/1; 224/3  
A:Superfamily: glycinin

Query Match	22.4%	Score 79.5	DB 2:	Length 236;
Best Local Similarity	33.3%	Pred. 0.021;		
Matches	17;	Conservative	8;	Mismatches 21; Indels 5; Gaps 1;

  

Oy	12	CRRCEQDEPQHOCCLCRCEQOQHOGGGMNPPQGGSGRYEEGEEQ	62
	40	CVRRCEDEPWHORPCLECCREEEESRHEAD-----SSGESSSSDEERK	85

RESULT 10  
T29475  
hypothetical protein T01D1.6 - *Caenorhabditis elegans*

C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
C:Accession: T29475  
R:Bradshaw, H.; Wohldmann, P.  
Submitted to the EMBL Data Library, November 1996  
A:Description: The sequence of C. elegans cosmid T01D1.  
A:Reference number: Z20623  
A:Accession: T29475  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-411 <BR>  
A:Cross-references: EMBL:U080455; PIDN:AA837887.1; GSPDB:GN00020; CESP:T01D1.6  
A:Experimental source: strain Bristol N2; clone T01D1  
C:Genetics:  
A:Gene: CESP:T01D1.6  
A:Map position: 2  
A:Introns: 25/3; 304/3  
C:Superfamily: gliadin

Query Match 22.3%; Score 79; DB 2; Length 411;  
Best Local Similarity 30.0%; Pred. No. 0.38;  
Matches 21; Conservative 12; Mismatches 23; Indels 14; Gaps 4;

OY 5 QQRREDCRRRC-EQOPRO--QHOCGLRCRE-----QQRHGRGDMNPNRQGS 52  
11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 :  
Db 142 QQQQQQCCQAACPPQQQQQQCCCTTCQSDQYSQQLIQDTYAQPQI--PAYTGR 199

OY 53 GRYEGEGEEQ 62  
1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 :  
Db 200 SEVTAPPOQ 209

RESULT 11  
A39248  
androgen receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 04-Oct-1991 #sequence\_revision 04-Oct-1991 #text\_change 24-Nov-1999  
C:Accession: A39248; A30328; A40109; A60946; A34942; A27653; A40108; A40494; A32224; A40  
R:Lubahn, D.B.; Brown, T.R.; Simental, J.A.; Higgs, H.N.; Migeon, C.J.; Wilson, E.M.; Fu  
Proc. Natl. Acad. Sci. U.S.A. 86, 9534-9538, 1989  
A:Title: Sequence of the Intron/exon junctions of the coding region of the human androge  
A:Reference number: A39248; MUID:90083302  
A:Accession: A39248  
A:Molecule type: DNA  
A:Residues: 1-919 <LUB>  
A:Cross-references: GB:M27423; GB:M27430; NID:9178904; PIDN:AA51886.1; PID:9178906  
R:Faber, P.W.; Kuiper, G.G.J.M.; van Rooij, H.C.J.; van der Korpuit, J.A.G.M.; Brinkmann,  
Mol. Cell. Endocrinol. 61, 257-262, 1989  
A:Title: The N-terminal domain of the human androgen receptor is encoded by one, large e  
A:Reference number: A30328; MUID:89137730  
A:Accession: A30328  
A:Molecule type: DNA  
A:Residues: 1-77, 79-165, 'A', 167-389, 'L', 391-464, 473-538 <FAB>  
A:Cross-references: GB:M20260  
R:Lubahn, D.B.; Joseph, D.R.; Sullivan, P.M.; Willard, H.F.; French, F.S.; Wilson, E.M.  
Science 240, 327-330, 1988  
A:Title: Cloning of human androgen receptor complementary DNA and localization to the X  
A:Reference number: A40109; MUID:88178112  
A:Accession: A40109  
A:Molecule type: DNA  
A:Residues: 559-624 <LUB>  
A:Cross-references: GB:M20132  
R:Kuiper, G.G.J.M.; Faber, P.W.; van Rooij, H.C.J.; van der Korpuit, J.A.G.M.; Ris-Stalpe  
J. Mol. Endocrinol. 2, R1-R4, 1989  
A:Title: Structural organization of the human androgen receptor gene.  
A:Reference number: A60946; MUID:89322749  
A:Accession: A60946  
A:Molecule type: DNA  
A:Residues: 536-540; 587-591; 626-631; 723-726; 770-774; 814-818; 867-870 <KUI>  
R:Lubahn, D.B.; Joseph, D.R.; Sar, M.; Tan, J.; Higgs, H.N.; Larson, R.E.; French, F.S.;  
Mol. Endocrinol. 2, 1265-1275, 1988  
A:Title: The human androgen receptor: complementary deoxyribonucleic acid cloning, sequ

A:Reference number: A34942; MUID:89112208  
A:Accession: A34942  
A:Molecule type: mRNA  
A:Residues: 1-919 <LUB>  
A:Cross-references: GB:M20132; NID:9178627; PIDN:AA51729.1; PID:9178628; GB:J03180  
R:Trappan, J.; Klaassen, P.; Kuiper, G.G.J.M.; van der Korpuit, J.A.G.M.; Faber, P.W.;  
Biochem. Biophys. Res. Commun. 153, 241-248, 1988  
A:Title: Cloning, structure and expression of a cDNA encoding the human androgen rece  
A:Reference number: A27653; MUID:88240407  
A:Accession: A27653  
A:Molecule type: mRNA  
A:Residues: 468-564, 'K', 566-919 <TRA>  
A:Cross-references: GB:M20260; NID:9178891; PIDN:AA51774.1; PID:9178892  
A:Note: the authors translated the codon AAG for residue 565 as Glu  
R:Chang, C.; Kokontis, J.; Liao, S.  
Science 240, 324-326, 1988  
A:Title: Molecular cloning of human and rat complementary DNA encoding androgen rece  
A:Reference number: A40108; MUID:88178111  
A:Accession: A40108  
A:Molecule type: mRNA  
A:Residues: 557-628 <CHA>  
A:Cross-references: GB:M18624  
R:Chang, C.; Kokontis, J.; Liao, S.  
Proc. Natl. Acad. Sci. U.S.A. 85, 7211-7215, 1988  
A:Title: Structural analysis of complementary DNA and amino acid sequences of human a  
A:Reference number: A40494; MUID:89017168  
A:Accession: A40494  
A:Molecule type: mRNA  
A:Residues: 1-74, 79-89, 'H', 90-472, 'GGG', 473-474, 'E', 476-644, 'N', 646-919 <CH2>  
A:Cross-references: GB:M23263  
R:Tilley, W.D.; Marcelli, M.; Wilson, J.D.; McPhaul, M.J.  
Proc. Natl. Acad. Sci. U.S.A. 86, 327-331, 1989  
A:Title: Characterization and expression of a cDNA encoding the human androgen recept  
A:Reference number: A32224; MUID:8908909  
A:Accession: A32224  
A:Molecule type: mRNA  
A:Residues: 1-77, 79-211, 'R', 213-471, 473-919 <TIL>  
A:Cross-references: GB:M21748; GB:J04150; NID:9178871; PIDN:AA51771.1; PID:9178872  
R:Kowalczyk, I.; Lee, H.J.; Chen, H.T.; Westlayer, C.; Portolis, M.C.; Cabrol, S.; Mau  
Mol. Endocrinol. 7, 861-869, 1993  
A:Title: A point mutation in the second zinc finger of the DNA-binding domain of the  
A:Reference number: A40715; MUID:94019395  
A:Accession: A40715  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 557-614, 'H', 616-624 <MOW>  
A:Cross-references: PIDN:AB28340.1; PID:9425580  
C:Genetics:  
A:Gene: GDB:AR  
A:Cross-references: GDB:120556; OMIM:313700  
A:Map position: Xq11-Xq12  
A:Introns: 538/2; 589/1; 628/1; 724/1; 772/2; 816/1; 868/3  
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology  
C:Keywords: DNA binding; steroid binding; transcription regulation; zinc finger  
F:557-815/Domain: erba transforming protein homology <ERBA>  
F:559-579/Region: zinc finger  
F:595-619/Region: zinc finger

Query Match 22.3%; Score 79; DB 2; Length 919;  
Best Local Similarity 32.8%; Pred. No. 0.78;  
Matches 19; Conservative 15; Mismatches 22; Indels 2; Gaps 1;

OY 5 QQRREDCRRRC-EQOPROQHOCGLRCRE--QQRHGRGDMNPNRQGSRYEGEGEEQ 62  
11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 :  
Db 58 QQQQQQ--QQQQQQQQQQQQQQQQQQQQQQGEGSPQAHRKPTGYLVDEQQ 113

RESULT 12  
S71628  
sensory transduction histidine kinase doka - slime mold (Dictyostelium discoideum)  
C:Species: Dictyostelium discoideum

C:Date: 27-Nov-1997 #sequence\_revision 12-Dec-1997 #text\_change 29-Oct-1999  
C:Accession: S71628; S78068  
R:Schuster, S.C.; Noegel, A.A.; Oehme, F.; Gerisch, G.; Simon, M.I.  
EMBO J. 15, 3880-3889, 1996  
A:Title: The hybrid histidine kinase Doka is part of the osmotic response system of *D. discoideum*  
A:Reference number: S71628; MUID:96324396  
A:Accession: S71628  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-1670 <SCH>  
A:Cross-references: EMBL:X96869  
A:Experimental source: strain AX2; substrain 214  
R:Schuster, S.C.; Noegel, A.A.; Oehme, F.; Gerisch, G.; Simon, M.I.  
submitted to the EMBL Data Library, March 1996  
A:Description: The hybrid histidine kinase Doka is part of the osmotic response system of *D. discoideum*  
A:Reference number: S78068  
A:Accession: S78068  
A:Molecule type: DNA  
A:Residues: 1-149, 'E', 151-219, 'TRVLKLIQSTNNMYWY', 238-1671 <SCW>  
A:Cross-references: EMBL:X96869; NID:g1237201; PID:CAA65612.1; PID:e233513; PID:g1237201  
C:Genetics:  
A:Gene: doka  
C:Function:  
A:Description: modulates cell response to changes in osmolarity; involved in spore formation  
C:Superfamily: response regulator homology  
C:Keywords: phosphoprotein; signal transduction  
E:1530-1629/Domain: response regulator homology <RRH2>  
E:1568/Binding site: phosphate (asp) (covalent) #status predicted

	Query Match	22.0%;	Score 78;	DB 2;	Length 1671;	
	Best Local Similarity	27.8%;	Pred. No. 1.7;			
	Matches	20;	Conservative	15;	Mismatches	27;
					Indels	10;
					Gaps	2.
OY	1	KRDPOGREDECDRRRCOEOPROHOCOLCRCEODRO----	HGRGDMNNPORGSGS---	53		
	:	: :	:: :	:::	:: :	
Dd	148	QEDPPSSGOEEEPPLSQOOOEOEFOEOEOEGSKIKTEGGKGGEHEECGCGGEGE		207		
OY	54	--RYEGEGEEO	62			
	:	::  :	:			
Dd	208	GEORFKEGDDEE	219			

RESULT 13  
527770  
hypothetical protein 1 - African malaria mosquito (fragment)  
C:Species: Anopheles gambiae (African malaria mosquito)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Sep-1997  
C:Accession: S27770  
R:Besansky, N.J.; Paskewitz, S.M.; Mills-Hamm, D.M.; Collins, F.H.  
submitted to the EMBL Data Library, June 1992  
A:Description: Distinct families of site-specific retroposons occupy identical positions  
A:Reference number: S27770  
A:Accession: S27770  
A:Molecule type: DNA  
A:Residues: 1-613 <BES>  
A:Cross-references: EMBL:M93690; NID:g159615; PID:g159616

```

Query Match      21.8%; Score 77.5; Db 2; Length 613;
Best Local Similarity 28.4%; Pred. No. 0.78;
Matches 19; Conservative 17; Mismatches 22; Indels 9; Gaps 2.

OY 1 KRDPQREYEDRCRCRCEOEPRQCH-----CQLKRCREQQRHGRGGGDMNMRGSGRY 55
   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 245 0000000000000000000000000000000000000000000000000000000000
      0000000000000000000000000000000000000000000000000000000000
OY 56 EDEEEEO 62
   ::::|:::|
Db 301 0000EOO 307
      0000000000000000000000000000000000000000000000000000000000

```

## RESULT 14

A34721  
androgen receptor A - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 12-Sep-1997  
C:Accession: A34721  
R:Govindan, M.V.  
Mol. Endocrinol. 4, 417-427, 1990  
A:Title: Specific region in hormone binding domain is essential for hormone binding a  
A:Reference number: A34721; MUID:90256935  
A:Accession: A34721  
A:Molecule type: mRNA  
A:Residues: 1-910 <GGCV>  
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology  
C:Keywords: zinc finger  
F:548-806/Domain: erba transforming protein homology <ERBA>  
F:550-570/Region: zinc finger  
F:586-610/Region: zinc finger

[illegible]

```

RESULT      15
B34721
androgen receptor B - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 12-Sep-1997
C:Accession: B34721

```

Mol. Endocrinol. 4, 417-427, 1990  
A:Title: Specific region in hormone binding domain is essential for hormone binding  
A:Reference number: A34721; MUID:90258935  
A:Accession: B34721  
A:Molecule type: mRNA  
A:Residues: 1-911 <GC02>  
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology  
C:Keywords: zinc finger  
F:348-806/Domain: erba transforming protein homology <ERBA>  
F:550-570/Region: zinc finger  
F:586-610/Region: zinc finger

```

Query Match          21.8%; Score 77.5; DB 2; Length 911;
Best Local Similarity 32.8%; Pred. No. 1.1;
Matches 19; Conservative 14; Mismatches 22; Indels 3; Gaps 1;

Oy 5 GQREVEDCRRRCDEQDEPRQCHCQCLRCQEQCHQHGRCGDMMPQGGSGRYVEGEEQ 62
Db 58 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 112
    ---:---:---:---:---:---:---:---:---:---:---:---:---:---:---:

```

Search completed: March 1, 2001, 15:52:23  
Job time: 547 sec

## RESULT 14

